SEQUENCE LISTING

<110> SUN..Y LIMITED

coding for a protein having glycosyl transferase

<120> aurone

< 1

1> 1751

12> DNA

213> Antirrhinum majus

<220>
<223> Nucleotide sequence coding for a protein having
glycosyl transferase to aurone

<400> 1

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ctcacttagt actaaaacac aaaactgaga acccttcaaa tttccacttg atcatattca    60
attttccttt taaaa atg gga aaa ctt cac att gcc tta ttt cca gtt atg    111
                 Met Gly Lys Leu His Ile Ala Leu Phe Pro Val Met
                   1               5                  10

gct cat ggt cac atg atc cca atg ttg gac atg gcc aag ctc ttt acc    159
Ala His Gly His Met Ile Pro Met Leu Asp Met Ala Lys Leu Phe Thr
             15                  20                  25

tca aga ggc ata caa aca aca atc att tcg act ctc gcc ttc gct gat    207
Ser Arg Gly Ile Gln Thr Thr Ile Ile Ser Thr Leu Ala Phe Ala Asp
         30                  35                  40

ccg ata aac aaa gct cgt gat tcg ggc ctc gat att gga cta agc atc    255
Pro Ile Asn Lys Ala Arg Asp Ser Gly Leu Asp Ile Gly Leu Ser Ile
     45                  50                  55                  60

ctc aaa ttc cca cca gaa gga tca gga ata cca gat cac atg gtg agc    303
Leu Lys Phe Pro Pro Glu Gly Ser Gly Ile Pro Asp His Met Val Ser
                 65                  70                  75
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ctt gat cta gtt act gaa gat tgg ctc cca aag ttt gtt gag tca tta      351
Leu Asp Leu Val Thr Glu Asp Trp Leu Pro Lys Phe Val Glu Ser Leu
              80                      85                  90

gtc tta tta caa gag cca gtt gag aag ctt atc gaa gaa cta aag ctc      399
Val Leu Leu Gln Glu Pro Val Glu Lys Leu Ile Glu Glu Leu Lys Leu
              95                  100                 105

gac tgt ctc gtt tcc gac atg ttc ttg cct tgg aca gtc gat tgt gcg      447
Asp Cys Leu Val Ser Asp Met Phe Leu Pro Trp Thr Val Asp Cys Ala
         110                 115                 120

gct aag ttc ggt att ccg agg ttg gtt ttc cac gga acg agc aac ttt      495
Ala Lys Phe Gly Ile Pro Arg Leu Val Phe His Gly Thr Ser Asn Phe
125                 130                 135                 140

gcg ttg tgt gct tcg gag caa atg aag ctt cac aag cct tat aag aat      543
Ala Leu Cys Ala Ser Glu Gln Met Lys Leu His Lys Pro Tyr Lys Asn
              145                 150                 155

gta act tct gat act gag aca ttt gtt ata ccg gat ttc ccg cat gag      591
Val Thr Ser Asp Thr Glu Thr Phe Val Ile Pro Asp Phe Pro His Glu
              160                 165                 170

ctg aag ttt gtg agg act caa gtg gct ccg ttt cag ctt gcg gaa acg      639
Leu Lys Phe Val Arg Thr Gln Val Ala Pro Phe Gln Leu Ala Glu Thr
         175                 180                 185

gag aat gga ttc tca aag ttg atg aaa cag atg acg gag tct gtt ggt      687
Glu Asn Gly Phe Ser Lys Leu Met Lys Gln Met Thr Glu Ser Val Gly
         190                 195                 200

aga agc tac ggt gtt gtg gtt aac agt ttt tat gag ctc gag tcg act      735
Arg Ser Tyr Gly Val Val Val Asn Ser Phe Tyr Glu Leu Glu Ser Thr
205                 210                 215                 220

tat gtg gat tat tac aga gag gtt ttg ggt aga aag tct tgg aat ata      783
Tyr Val Asp Tyr Tyr Arg Glu Val Leu Gly Arg Lys Ser Trp Asn Ile
              225                 230                 235

ggg cct ctg ttg tta tcc aac aat ggc aat gag gaa aaa gta caa agg      831
Gly Pro Leu Leu Leu Ser Asn Asn Gly Asn Glu Glu Lys Val Gln Arg
              240                 245                 250

gga aag gaa tct gcg att ggc gaa cac gaa tgc ttg gct tgg ttg aat      879
Gly Lys Glu Ser Ala Ile Gly Glu His Glu Cys Leu Ala Trp Leu Asn
              255                 260                 265
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tcc aag aag cag aat tcg gtt gtt tac gtt tgt ttt gga agt atg gcg      927
Ser Lys Lys Gln Asn Ser Val Val Tyr Val Cys Phe Gly Ser Met Ala
    270                 275                 280

act ttt act cca gcg cag ttg cgc gaa act gcg att gga ctc gag gaa      975
Thr Phe Thr Pro Ala Gln Leu Arg Glu Thr Ala Ile Gly Leu Glu Glu
285                 290                 295                 300

tca ggc caa gag ttc att tgg gta gtt aaa aag gcc aaa aac gaa gaa     1023
Ser Gly Gln Glu Phe Ile Trp Val Val Lys Lys Ala Lys Asn Glu Glu
                305                 310                 315

gaa gga aaa gga aaa gaa gaa tgg ctg cca gaa aat ttt gag gaa aga     1071
Glu Gly Lys Gly Lys Glu Glu Trp Leu Pro Glu Asn Phe Glu Glu Arg
                320                 325                 330

gtg aaa gat aga ggc ttg atc ata aga gga tgg gcg ccg caa ttg ttg     1119
Val Lys Asp Arg Gly Leu Ile Ile Arg Gly Trp Ala Pro Gln Leu Leu
                335                 340                 345

ata ctc gat cat cct gcg gta gga gct ttc gtg acg cat tgt gga tgg     1167
Ile Leu Asp His Pro Ala Val Gly Ala Phe Val Thr His Cys Gly Trp
    350                 355                 360

aat tcg acg ttg gaa gga ata tgc gcc ggt gtg cct atg gtg act tgg     1215
Asn Ser Thr Leu Glu Gly Ile Cys Ala Gly Val Pro Met Val Thr Trp
365                 370                 375                 380

cca gtt ttc gca gag cag ttt ttc aat gag aag ttt gtg aca gag gtt     1263
Pro Val Phe Ala Glu Gln Phe Phe Asn Glu Lys Phe Val Thr Glu Val
                385                 390                 395

ttg ggg acc ggt gtt tcg gtt ggg aat aag aag tgg cta agg gca gca     1311
Leu Gly Thr Gly Val Ser Val Gly Asn Lys Lys Trp Leu Arg Ala Ala
                400                 405                 410

agt gaa ggt gtg tcg agg gag gca gtg acg aac gcg gtg cag cgt gtt     1359
Ser Glu Gly Val Ser Arg Glu Ala Val Thr Asn Ala Val Gln Arg Val
    415                 420                 425

atg gtg gga gaa aat gcg tcg gag atg aga aag cga gcg aag tat tat     1407
Met Val Gly Glu Asn Ala Ser Glu Met Arg Lys Arg Ala Lys Tyr Tyr
    430                 435                 440

aag gaa atg gcg agg cgg gcg gtt gag gaa ggc ggt tcg tct tat aat     1455
Lys Glu Met Ala Arg Arg Ala Val Glu Glu Gly Gly Ser Ser Tyr Asn
445                 450                 455                 460
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ggt ttg aat gag atg ata gag gat ttg agt gtg tac cgt gct cca gaa    1503
Gly Leu Asn Glu Met Ile Glu Asp Leu Ser Val Tyr Arg Ala Pro Glu
                      465                 470                 475
aaa caa gac tta aac tagattctta tagatgactt ctagtgtgac aattgtaatt   1558
Lys Gln Asp Leu Asn
              480
ttttgccttt tattcaagtt tcctcattag tgttgagagc tttccctgta ttttcagaat 1618
tggtttgttc aatttttaca tgatttgtga tagatagctg catagtttct agctgttaac 1678
attgtttgat catattgagt tgatttaaaa tgagagtagc atgtgatctt cagattaaaa 1738
aaaaaaaaaa aaa                                                     1751
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<210> 2
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<213> Antirrhinum majus

<220>
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      transferase to aurone

<400> 2
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Met Ile Pro Met Leu Asp Met Ala Lys Leu Phe Thr Ser Arg Gly Ile
              20                  25                  30
Gln Thr Thr Ile Ile Ser Thr Leu Ala Phe Ala Asp Pro Ile Asn Lys
          35                  40                  45
Ala Arg Asp Ser Gly Leu Asp Ile Gly Leu Ser Ile Leu Lys Phe Pro
      50                  55                  60
Pro Glu Gly Ser Gly Ile Pro Asp His Met Val Ser Leu Asp Leu Val
  65                  70                  75                  80
Thr Glu Asp Trp Leu Pro Lys Phe Val Glu Ser Leu Val Leu Leu Gln
              85                  90                  95
Glu Pro Val Glu Lys Leu Ile Glu Glu Leu Lys Leu Asp Cys Leu Val
             100                 105                 110
Ser Asp Met Phe Leu Pro Trp Thr Val Asp Cys Ala Ala Lys Phe Gly
             115                 120                 125
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Ile Pro Arg Leu Val Phe His Gly Thr Ser Asn Phe Ala Leu Cys Ala
    130   135   140

Ser Glu Gln Met Lys Leu His Lys Pro Tyr Lys Asn Val Thr Ser Asp
145   150   155   160

Thr Glu Thr Phe Val Ile Pro Asp Phe Pro His Glu Leu Lys Phe Val
                165   170   175

Arg Thr Gln Val Ala Pro Phe Gln Leu Ala Glu Thr Glu Asn Gly Phe
                180   185   190

Ser Lys Leu Met Lys Gln Met Thr Glu Ser Val Gly Arg Ser Tyr Gly
            195   200   205

Val Val Val Asn Ser Phe Tyr Glu Leu Glu Ser Thr Tyr Val Asp Tyr
    210   215   220

Tyr Arg Glu Val Leu Gly Arg Lys Ser Trp Asn Ile Gly Pro Leu Leu
225   230   235   240

Leu Ser Asn Asn Gly Asn Glu Glu Lys Val Gln Arg Gly Lys Glu Ser
                245   250   255

Ala Ile Gly Glu His Glu Cys Leu Ala Trp Leu Asn Ser Lys Lys Gln
                260   265   270

Asn Ser Val Val Tyr Val Cys Phe Gly Ser Met Ala Thr Phe Thr Pro
            275   280   285

Ala Gln Leu Arg Glu Thr Ala Ile Gly Leu Glu Glu Ser Gly Gln Glu
        290   295   300

Phe Ile Trp Val Val Lys Lys Ala Lys Asn Glu Glu Glu Gly Lys Gly
305   310   315   320

Lys Glu Glu Trp Leu Pro Glu Asn Phe Glu Glu Arg Val Lys Asp Arg
                325   330   335

Gly Leu Ile Ile Arg Gly Trp Ala Pro Gln Leu Leu Ile Leu Asp His
                340   345   350

Pro Ala Val Gly Ala Phe Val Thr His Cys Gly Trp Asn Ser Thr Leu
            355   360   365

Glu Gly Ile Cys Ala Gly Val Pro Met Val Thr Trp Pro Val Phe Ala
        370   375   380

Glu Gln Phe Phe Asn Glu Lys Phe Val Thr Glu Val Leu Gly Thr Gly
385   390   395   400

Val Ser Val Gly Asn Lys Lys Trp Leu Arg Ala Ala Ser Glu Gly Val
                405   410   415

Ser Arg Glu Ala Val Thr Asn Ala Val Gln Arg Val Met Val Gly Glu
                420   425   430

Asn Ala Ser Glu Met Arg Lys Arg Ala Lys Tyr Tyr Lys Glu Met Ala
        435   440   445

Arg Arg Ala Val Glu Glu Gly Gly Ser Ser Tyr Asn Gly Leu Asn Glu
        450   455   460

Met Ile Glu Asp Leu Ser Val Tyr Arg Ala Pro Glu Lys Gln Asp Leu
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Asn

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ataactacat atgggacaac tccac   25

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cagaacagga tccacacgta attta   25

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ataactacat atgggaaaac ttcac   25

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gaacaggatc cacacactag aagtca   26

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<212> DNA
<213> Petunia hybrida

<220>
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      glycosyl transferase to aurone

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ccaaattctc tgatctttcc actaataatt tccca atg gct att ccc aca gtg   53
                                       Met Ala Ile Pro Thr Val
                                        1   5

caa cca cat ttt gtg ctg ctt cct ttc atg gca caa ggc cat aca aat 101
Gln Pro His Phe Val Leu Leu Pro Phe Met Ala Gln Gly His Thr Asn
            10   15   20

ccc atg att gac atc gca cgc cta ttg gca caa cgc gga gtt ata atc 149
Pro Met Ile Asp Ile Ala Arg Leu Leu Ala Gln Arg Gly Val Ile Ile
        25   30   35

acc att ctt act aca cac ttt aat gcc act aga ttc aag aca gtc gtt 197
Thr Ile Leu Thr Thr His Phe Asn Ala Thr Arg Phe Lys Thr Val Val
    40   45   50

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gat cgg gca gta gtg gca gca cta aag att cag gta gtt cac ctc tat    245
Asp Arg Ala Val Val Ala Ala Leu Lys Ile Gln Val Val His Leu Tyr
55                   60              65              70

ttt cca agc tta gag gct gga cta cct gaa ggg tgt gaa gct ttc gac    293
Phe Pro Ser Leu Glu Ala Gly Leu Pro Glu Gly Cys Glu Ala Phe Asp
                75              80              85

atg ctt cct tca atg gat ttc gca atg aaa ttc ttt gat gct acc agt    341
Met Leu Pro Ser Met Asp Phe Ala Met Lys Phe Phe Asp Ala Thr Ser
                90              95              100

agg ctt caa cca caa gtg gaa gaa atg ctt cat gaa ctg caa ccg tca    389
Arg Leu Gln Pro Gln Val Glu Glu Met Leu His Glu Leu Gln Pro Ser
            105             110             115

cca agt tgc ata ata tct gat atg tgt ttt cca tgg aca act aat gtt    437
Pro Ser Cys Ile Ile Ser Asp Met Cys Phe Pro Trp Thr Thr Asn Val
            120             125             130

gca caa aaa ttc aac att cct agg ctt gtt ttt cat ggg atg tgc tgt    485
Ala Gln Lys Phe Asn Ile Pro Arg Leu Val Phe His Gly Met Cys Cys
135             140             145             150

ttt tct tta ttg tgc ttg cac aat ttg aga gat tgg aag gag ttg gag    533
Phe Ser Leu Leu Cys Leu His Asn Leu Arg Asp Trp Lys Glu Leu Glu
                155             160             165

tct gat ata gaa tat ttt caa gtt cca gga tta cat gac aaa att gaa    581
Ser Asp Ile Glu Tyr Phe Gln Val Pro Gly Leu His Asp Lys Ile Glu
                170             175             180

tta aac aaa gct cag ctt tca aat att gtt aag cca aga ggt cct gat    629
Leu Asn Lys Ala Gln Leu Ser Asn Ile Val Lys Pro Arg Gly Pro Asp
                185             190             195

tgg aat gaa ttt gca gat caa ctg aag aaa gca gaa gaa gaa gct tat    677
Trp Asn Glu Phe Ala Asp Gln Leu Lys Lys Ala Glu Glu Glu Ala Tyr
                200             205             210

ggg ata gta gct aat agc ttt gaa gag tta gaa cca gaa tat gtc aag    725
Gly Ile Val Ala Asn Ser Phe Glu Glu Leu Glu Pro Glu Tyr Val Lys
215             220             225             230

gga ttg gaa aag gca aaa ggc ttg aaa att tgg cca att ggt cct gtt    773
Gly Leu Glu Lys Ala Lys Gly Leu Lys Ile Trp Pro Ile Gly Pro Val
            235             240             245
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tct ttg tgc aac aaa gag aaa cag gac aag gct gaa aga gga aac aag    821
Ser Leu Cys Asn Lys Glu Lys Gln Asp Lys Ala Glu Arg Gly Asn Lys
            250              255              260

gct tca att gat gaa cac cag tgt cta aaa tgg cta gat tct tgg gga    869
Ala Ser Ile Asp Glu His Gln Cys Leu Lys Trp Leu Asp Ser Trp Gly
            265              270              275

gca aac tct gta ctc ttt gta tgt ctc ggg agc cta tcg cgc ctt cca    917
Ala Asn Ser Val Leu Phe Val Cys Leu Gly Ser Leu Ser Arg Leu Pro
            280              285              290

acg cca caa atg ata gag ctg gga ctt ggc tta gaa tcg tcg aaa aga    965
Thr Pro Gln Met Ile Glu Leu Gly Leu Gly Leu Glu Ser Ser Lys Arg
295              300              305              310

ccc ttt att tgg gtt gtt aga cac aag tca gat gaa ttt aaa agt tgg    1013
Pro Phe Ile Trp Val Val Arg His Lys Ser Asp Glu Phe Lys Ser Trp
            315              320              325

cta gtt gaa gaa aat ttt gag gaa aga gtt aaa gga caa gga ctt tta    1061
Leu Val Glu Glu Asn Phe Glu Glu Arg Val Lys Gly Gln Gly Leu Leu
            330              335              340

atc cat ggt tgg gca cca caa gta cta ata tta tct cac act tca att    1109
Ile His Gly Trp Ala Pro Gln Val Leu Ile Leu Ser His Thr Ser Ile
            345              350              355

gga gga ttc ttg act cat tgt gga tgg aat tcg agt gtc gaa gga ata    1157
Gly Gly Phe Leu Thr His Cys Gly Trp Asn Ser Ser Val Glu Gly Ile
            360              365              370

tct gca ggc gtt cca atg atc act tgg cca atg ttt gct gaa caa ttc    1205
Ser Ala Gly Val Pro Met Ile Thr Trp Pro Met Phe Ala Glu Gln Phe
375              380              385              390

tgt aat gaa agg cta ata gtg aat gta ctg aag aca gga gta aag gct    1253
Cys Asn Glu Arg Leu Ile Val Asn Val Leu Lys Thr Gly Val Lys Ala
            395              400              405

gga att gag aat cct gtt atg ttt gga gag gaa gaa aaa gtt gga gca    1301
Gly Ile Glu Asn Pro Val Met Phe Gly Glu Glu Glu Lys Val Gly Ala
            410              415              420

caa gtg agc aaa gat gat att aag atg gtt att gaa aga gtc atg ggc    1349
Gln Val Ser Lys Asp Asp Ile Lys Met Val Ile Glu Arg Val Met Gly
            425              430              435
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gaa gaa gag gaa gct gaa atg aga aga aaa aga gca aaa gag tta gga    1397
Glu Glu Glu Glu Ala Glu Met Arg Arg Lys Arg Ala Lys Glu Leu Gly
    440                 445                 450

gaa aag gca aag agg gct atg gag gaa ggg ggt tcc tca cac ttc aac    1445
Glu Lys Ala Lys Arg Ala Met Glu Glu Gly Gly Ser Ser His Phe Asn
455                 460                 465                 470

ttg aca cag ttg att caa gat gtc act gag caa gca aat att tta aaa    1493
Leu Thr Gln Leu Ile Gln Asp Val Thr Glu Gln Ala Asn Ile Leu Lys
                475                 480                 485

tcc atc taggattata aagtcgattc caagttcctt ttacgatcaa tttctaacca    1549
Ser Ile

tctactagag atggtaacaa tccaaactgc gcctttttg cacaataatt attgttttat 1609
gttcagctag cacaaaaagt ttactattag tagaaatatt tcagctggaa ctgccgaact 1669
gctatgtaca ctgatggaac aatgtatgtc atgctattca aattaactct gagctgaaaa 1729
                                                                  1750
tatcatatag gagctgattt t


<210> 8
<211> 488
<212> PRT
<213> Petunia hybrida


<220>
<223> Amino acid sequence of a protein having glycosyl
      transferase to aurone


<400> 8
Met Ala Ile Pro Thr Val Gln Pro His Phe Val Leu Leu Pro Phe Met
  1                 5                  10                  15
Ala Gln Gly His Thr Asn Pro Met Ile Asp Ile Ala Arg Leu Leu Ala
                20                  25                  30
Gln Arg Gly Val Ile Ile Thr Ile Leu Thr Thr His Phe Asn Ala Thr
            35                  40                  45
Arg Phe Lys Thr Val Val Asp Arg Ala Val Val Ala Ala Leu Lys Ile
        50                  55                  60
Gln Val Val His Leu Tyr Phe Pro Ser Leu Glu Ala Gly Leu Pro Glu
    65                  70                  75                  80
Gly Cys Glu Ala Phe Asp Met Leu Pro Ser Met Asp Phe Ala Met Lys
                85                  90                  95
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Phe Phe Asp Ala Thr Ser Arg Leu Gln Pro Gln Val Glu Glu Met Leu
        100                 105                 110

His Glu Leu Gln Pro Ser Pro Ser Cys Ile Ile Ser Asp Met Cys Phe
        115                 120                 125

Pro Trp Thr Thr Asn Val Ala Gln Lys Phe Asn Ile Pro Arg Leu Val
        130                 135                 140

Phe His Gly Met Cys Cys Phe Ser Leu Leu Cys Leu His Asn Leu Arg
145                 150                 155                 160

Asp Trp Lys Glu Leu Glu Ser Asp Ile Glu Tyr Phe Gln Val Pro Gly
                165                 170                 175

Leu His Asp Lys Ile Glu Leu Asn Lys Ala Gln Leu Ser Asn Ile Val
            180                 185                 190

Lys Pro Arg Gly Pro Asp Trp Asn Glu Phe Ala Asp Gln Leu Lys Lys
            195                 200                 205

Ala Glu Glu Glu Ala Tyr Gly Ile Val Ala Asn Ser Phe Glu Glu Leu
        210                 215                 220

Glu Pro Glu Tyr Val Lys Gly Leu Glu Lys Ala Lys Gly Leu Lys Ile
225                 230                 235                 240

Trp Pro Ile Gly Pro Val Ser Leu Cys Asn Lys Glu Lys Gln Asp Lys
                245                 250                 255

Ala Glu Arg Gly Asn Lys Ala Ser Ile Asp Glu His Gln Cys Leu Lys
            260                 265                 270

Trp Leu Asp Ser Trp Gly Ala Asn Ser Val Leu Phe Val Cys Leu Gly
            275                 280                 285

Ser Leu Ser Arg Leu Pro Thr Pro Gln Met Ile Glu Leu Gly Leu Gly
        290                 295                 300

Leu Glu Ser Ser Lys Arg Pro Phe Ile Trp Val Val Arg His Lys Ser
305                 310                 315                 320

Asp Glu Phe Lys Ser Trp Leu Val Glu Glu Asn Phe Glu Glu Arg Val
                325                 330                 335

Lys Gly Gln Gly Leu Leu Ile His Gly Trp Ala Pro Gln Val Leu Ile
            340                 345                 350

Leu Ser His Thr Ser Ile Gly Gly Phe Leu Thr His Cys Gly Trp Asn
            355                 360                 365

Ser Ser Val Glu Gly Ile Ser Ala Gly Val Pro Met Ile Thr Trp Pro
        370                 375                 380

Met Phe Ala Glu Gln Phe Cys Asn Glu Arg Leu Ile Val Asn Val Leu
385                 390                 395                 400
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Lys Thr Gly Val Lys Ala Gly Ile Glu Asn Pro Val Met Phe Gly Glu
                405   410   415

Glu Glu Lys Val Gly Ala Gln Val Ser Lys Asp Asp Ile Lys Met Val
                420   425   430

Ile Glu Arg Val Met Gly Glu Glu Glu Glu Ala Glu Met Arg Arg Lys
                435   440   445

Arg Ala Lys Glu Leu Gly Glu Lys Ala Lys Arg Ala Met Glu Glu Gly
        450   455   460

Gly Ser Ser His Phe Asn Leu Thr Gln Leu Ile Gln Asp Val Thr Glu
465   470   475   480

Gln Ala Asn Ile Leu Lys Ser Ile
                    485

<210> 9
<211> 1669
<212> DNA
<213> Petunia hybrida

<220>
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      glycosyl transferase to aurone

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tgctaagtac tactactagt acacatcttt ctttctatca aacactttcc aaa atg   116
                                                              Met
                                                                1

ggt cag ctc cat ttt ttc ttc ttt ccc atg atg gct cat ggc cac atg   164
Gly Gln Leu His Phe Phe Phe Phe Pro Met Met Ala His Gly His Met
                5   10   15

att cct aca cta gac atg gct aag ctt ttc gct tca cgt ggt gtt aag   212
Ile Pro Thr Leu Asp Met Ala Lys Leu Phe Ala Ser Arg Gly Val Lys
                20   25   30

gcc acc ata atc act act cct ctc aat gaa tca gtt ttc tcc aaa gct   260
Ala Thr Ile Ile Thr Thr Pro Leu Asn Glu Ser Val Phe Ser Lys Ala
        35   40   45

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att gaa aga aac aag cat gaa att gac atc cgt ttg atc aaa ttc caa      308
Ile Glu Arg Asn Lys His Glu Ile Asp Ile Arg Leu Ile Lys Phe Gln
 50               55               60               65

gct gtt gaa aat ggc ttg cct gaa ggt tgt gag cgt att gat ctt atc      356
Ala Val Glu Asn Gly Leu Pro Glu Gly Cys Glu Arg Ile Asp Leu Ile
                 70               75               80

cct tct gat gac aag ctt tcc aat ttt ttg aaa gct gca gct atg atg      404
Pro Ser Asp Asp Lys Leu Ser Asn Phe Leu Lys Ala Ala Ala Met Met
                 85               90               95

caa gaa cca ctt gag cag ctt att gaa gaa tgt cat ccc aat tgt ctt      452
Gln Glu Pro Leu Glu Gln Leu Ile Glu Glu Cys His Pro Asn Cys Leu
            100              105              110

gtt tct gat atg ttc ctt cct tgg act act gat act gca gcc aag ttt      500
Val Ser Asp Met Phe Leu Pro Trp Thr Thr Asp Thr Ala Ala Lys Phe
            115              120              125

aac att cca aga ata gtt ttc cat ggt acg agt ttc ttt gca ctt tgt      548
Asn Ile Pro Arg Ile Val Phe His Gly Thr Ser Phe Phe Ala Leu Cys
130              135              140              145

gta gag aat agt aac agg act aat aag cca ttc aag aac gtc tct tct      596
Val Glu Asn Ser Asn Arg Thr Asn Lys Pro Phe Lys Asn Val Ser Ser
            150              155              160

gat tct gaa act ttt gtt gta cca aat ttg cct cac gaa atc agg cta      644
Asp Ser Glu Thr Phe Val Val Pro Asn Leu Pro His Glu Ile Arg Leu
            165              170              175

act aga aca caa ttg tct ccg ttt gag caa tca ttg gaa gag aca cca      692
Thr Arg Thr Gln Leu Ser Pro Phe Glu Gln Ser Leu Glu Glu Thr Pro
            180              185              190

atg tcc cga atg ata aaa gca gtt agg gaa tcg gac gcg aag agt tat      740
Met Ser Arg Met Ile Lys Ala Val Arg Glu Ser Asp Ala Lys Ser Tyr
            195              200              205

gga gtt atc ttc aac agc ttc tat gag ctt gaa tca gat tat gtt gaa      788
Gly Val Ile Phe Asn Ser Phe Tyr Glu Leu Glu Ser Asp Tyr Val Glu
210              215              220              225

cat tat acc aag gtt ctt ggt aga aag tct tgg gct att ggc ccg ctt      836
His Tyr Thr Lys Val Leu Gly Arg Lys Ser Trp Ala Ile Gly Pro Leu
            230              235              240
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tct ttg tgc aat agg gac att gaa gat aaa gct gaa aga ggg aag att   884
Ser Leu Cys Asn Arg Asp Ile Glu Asp Lys Ala Glu Arg Gly Lys Ile
            245   250   255

tcc tct att gat aaa cat gag tgt ttg aat tgg ctt gat tca aag aaa   932
Ser Ser Ile Asp Lys His Glu Cys Leu Asn Trp Leu Asp Ser Lys Lys
            260   265   270

cca agt tcc att gtt tat gtt tgc ttc ggg agc gta gca gat ttc act   980
Pro Ser Ser Ile Val Tyr Val Cys Phe Gly Ser Val Ala Asp Phe Thr
            275   280   285

gca gca caa atg cgt gaa ctt gca ttg gga att gaa gca tct gga caa   1028
Ala Ala Gln Met Arg Glu Leu Ala Leu Gly Ile Glu Ala Ser Gly Gln
290   295   300   305

gaa ttc att tgg gct gtt aga aga ggc aaa gag gaa caa gac aat gaa   1076
Glu Phe Ile Trp Ala Val Arg Arg Gly Lys Glu Glu Gln Asp Asn Glu
            310   315   320

gag tgg ttg cct gaa gga ttc gag gaa aga acg aaa gaa aaa ggt cta   1124
Glu Trp Leu Pro Glu Gly Phe Glu Glu Arg Thr Lys Glu Lys Gly Leu
            325   330   335

att att aga gga tgg gcg ccc caa gtg cta att ctt gat cac caa gct   1172
Ile Ile Arg Gly Trp Ala Pro Gln Val Leu Ile Leu Asp His Gln Ala
            340   345   350

gtg gga gct ttt gtc act cat tgt ggt tgg aat tca acg ctt gaa gga   1220
Val Gly Ala Phe Val Thr His Cys Gly Trp Asn Ser Thr Leu Glu Gly
            355   360   365

gta tca gca ggg gtg cct atg gtg acc tgg cct gtg ttt gca gag caa   1268
Val Ser Ala Gly Val Pro Met Val Thr Trp Pro Val Phe Ala Glu Gln
370   375   380   385

ttt ttc aat gaa aag ttg gtg act gag gtt ttg aga act ggg gct ggt   1316
Phe Phe Asn Glu Lys Leu Val Thr Glu Val Leu Arg Thr Gly Ala Gly
            390   395   400

gtt ggt tca atg caa tgg aaa aga tca gct agc gag gga gta aaa agg   1364
Val Gly Ser Met Gln Trp Lys Arg Ser Ala Ser Glu Gly Val Lys Arg
            405   410   415

gaa gca ata gct aag gca ata aag aga gtc atg gtg agt gaa gaa gca   1412
Glu Ala Ile Ala Lys Ala Ile Lys Arg Val Met Val Ser Glu Glu Ala
            420   425   430

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gag gga ttc aga aac cga gct aaa gcc tac aaa gag atg gca aaa caa    1460
Glu Gly Phe Arg Asn Arg Ala Lys Ala Tyr Lys Glu Met Ala Lys Gln
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gct att gaa gaa gga gga tct tct tac tct gga ttg act act ttg cta    1508
Ala Ile Glu Glu Gly Gly Ser Ser Tyr Ser Gly Leu Thr Thr Leu Leu
450                 455                 460                 465

caa gat ata agt aca tat agt tcc aaa agt cat taactgcaca actaaaaaaa 1561
Gln Asp Ile Ser Thr Tyr Ser Ser Lys Ser His
                570                 475

tgtagtgttg ttctacaa tttttatgct ttttatgcg tgtactaatt taaacatgga   1621
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Lys Ala Thr Ile Ile Thr Thr Pro Leu Asn Glu Ser Val Phe Ser Lys
            35                  40                  45
Ala Ile Glu Arg Asn Lys His Glu Ile Asp Ile Arg Leu Ile Lys Phe
        50                  55                  60
Gln Ala Val Glu Asn Gly Leu Pro Glu Gly Cys Glu Arg Ile Asp Leu
    65                  70                  75                  80
Ile Pro Ser Asp Asp Lys Leu Ser Asn Phe Leu Lys Ala Ala Ala Met
                85                  90                  95
Met Gln Glu Pro Leu Glu Gln Leu Ile Glu Glu Cys His Pro Asn Cys
                100                 105                 110
Leu Val Ser Asp Met Phe Leu Pro Trp Thr Thr Asp Thr Ala Ala Lys
            115                 120                 125
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Phe Asn Ile Pro Arg Ile Val Phe His Gly Thr Ser Phe Phe Ala Leu
130 135 140

Cys Val Glu Asn Ser Asn Arg Thr Asn Lys Pro Phe Lys Asn Val Ser
145 150 155 160

Ser Asp Ser Glu Thr Phe Val Val Pro Asn Leu Pro His Glu Ile Arg
165 170 175

Leu Thr Arg Thr Gln Leu Ser Pro Phe Glu Gln Ser Leu Glu Glu Thr
180 185 190

Pro Met Ser Arg Met Ile Lys Ala Val Arg Glu Ser Asp Ala Lys Ser
195 200 205

Tyr Gly Val Ile Phe Asn Ser Phe Tyr Glu Leu Glu Ser Asp Tyr Val
210 215 220

Glu His Tyr Thr Lys Val Leu Gly Arg Lys Ser Trp Ala Ile Gly Pro
225 230 235 240

Leu Ser Leu Cys Asn Arg Asp Ile Glu Asp Lys Ala Glu Arg Gly Lys
245 250 255

Ile Ser Ser Ile Asp Lys His Glu Cys Leu Asn Trp Leu Asp Ser Lys
260 265 270

Lys Pro Ser Ser Ile Val Tyr Val Cys Phe Gly Ser Val Ala Asp Phe
275 280 285

Thr Ala Ala Gln Met Arg Glu Leu Ala Leu Gly Ile Glu Ala Ser Gly
290 295 300

Gln Glu Phe Ile Trp Ala Val Arg Arg Gly Lys Glu Glu Gln Asp Asn
305 310 315 320

Glu Glu Trp Leu Pro Glu Gly Phe Glu Glu Arg Thr Lys Glu Lys Gly
325 330 335

Leu Ile Ile Arg Gly Trp Ala Pro Gln Val Leu Ile Leu Asp His Gln
340 345 350

Ala Val Gly Ala Phe Val Thr His Cys Gly Trp Asn Ser Thr Leu Glu
355 360 365

Gly Val Ser Ala Gly Val Pro Met Val Thr Trp Pro Val Phe Ala Glu
370 375 380

Gln Phe Phe Asn Glu Lys Leu Val Thr Glu Val Leu Arg Thr Gly Ala
385 390 395 400

Gly Val Gly Ser Met Gln Trp Lys Arg Ser Ala Ser Glu Gly Val Lys
405 410 415

Arg Glu Ala Ile Ala Lys Ala Ile Lys Arg Val Met Val Ser Glu Glu
420 425 430

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Ala Glu Gly Phe Arg Asn Arg Ala Lys Ala Tyr Lys Glu Met Ala Lys
        435                 440                 445

Gln Ala Ile Glu Glu Gly Gly Ser Ser Tyr Ser Gly Leu Thr Thr Leu
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Leu Gln Asp Ile Ser Thr Tyr Ser Ser Lys Ser His
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